## Claims

Claims 1-19 (Canceled)


20. (Currently amended) A method for compensating for drift in fingerprint spectra due to ~~changes~~ differences in environmental factors that affect the metabolic state of microorganisms, comprising:

culturing under a first set of environmental factors a first microorganism ~~of interest~~ and a second microorganism that is presumably metabolically similar to the first microorganism ~~of interest~~;

measuring a fingerprint spectrum of the first microorganism ~~of interest~~ cultured under the first set of environmental factors and a fingerprint spectrum of the second microorganism cultured under the first set of environmental factors;

obtaining a fingerprint spectrum of the second microorganism cultured under a second set of environmental factors that differ from the first set of environmental factors and affect the metabolic state of the first and second microorganisms;

deriving a relationship ~~detecting differences~~ between the fingerprint spectrum of the second microorganism cultured under the first set of environmental factors and [[a]] the fingerprint spectrum of the second microorganism cultured under [[a]] the second set of environmental factors; and,

applying the relationship derived for the second microorganism ~~using the differences between the fingerprint spectra of the second microorganism cultured under the two sets of environmental factors~~ to transform the fingerprint spectrum of the first microorganism ~~of interest~~ cultured under the first set of environmental factors to an expected fingerprint spectrum for the first microorganism ~~of interest~~ under the second set of environmental factors that is compensated for drift due to the differences between the first and second sets of environmental factors that affect the metabolic state of the first microorganism.


21. (Withdrawn, currently amended) The method of claim 20 ~~where~~ wherein culturing under a first set of environmental factors comprises culturing on a test growth medium and culturing under the second set of environmental factors comprises culturing on a library growth medium that differs from the test growth medium.

22. (Currently amended) The method of claim 20 ~~where~~ <u>wherein</u> the fingerprint spectra are selected from the group consisting of mass spectra, electron impact mass spectra, pyrolysis mass spectra, MAB mass spectra, MALDI mass spectra, ESI mass spectra, infrared spectra, Fourier-transform infrared spectra, diffuse reflectance infrared spectra, attenuated total reflectance infrared spectra, ion-mobility spectra, gas chromatograms, fatty-acid methyl ester gas chromatograms, liquid chromatograms, and nuclear magnetic resonance spectra, and portions and combinations thereof.

23. (Currently amended) The method of claim 20 including a step of identifying the <u>first</u> microorganism ~~of interest~~ by detecting a similarity between the expected fingerprint spectrum for the <u>second</u> microorganism ~~of interest~~ and a fingerprint spectrum of a known organism cultured under the second set of environmental factors.

24. (Currently amended) The method of claim 23 ~~where~~ <u>wherein</u> detecting a similarity is accomplished by a pattern recognition method selected from the group consisting of statistical pattern recognition methods, artificial intelligence pattern recognition methods, and combinations thereof.

25. (Currently amended) The method of claim 20 ~~where using differences between the fingerprint spectra of the second microorganism cultured under the two sets of environmental factors to transform the fingerprint spectrum of the microorganism of interest to an expected fingerprint spectrum~~ <u>wherein the derived relationship</u> comprises ~~using~~ proportional differences in individual elements of the fingerprint spectra of the second microorganism between the first and second sets of environmental factors<u>.</u> ~~to transform the corresponding elements of the fingerprint spectrum of the microorganism of interest cultured under the first set of environmental factors into expected elements of a fingerprint spectrum for the microorganism of interest cultured under the second set of environmental factors.~~

26. (Currently amended) The method of claim 20 ~~where~~ <u>wherein</u> the <u>first</u> microorganism ~~of interest~~ is presumed to be a bacterium belonging to a certain class of physiologically similar bacteria and the <u>second,</u> presumably metabolically similar microorganism belongs to the same

class of physiologically similar bacteria, but the first and second microorganisms belong to different genera of bacteria of the same class of physiologically similar bacteria.

27. (Currently amended) The method of claim 20 ~~where~~ wherein the first microorganism ~~of interest~~ is presumed to be a bacterium belonging to a certain genus of bacteria and the second, presumably metabolically similar microorganism is of the same genus of bacteria, but the first and second microorganisms belong to different species of bacteria of the same genus of bacteria.

28. (Currently amended) The method of claim 20 ~~where~~ wherein the first microorganism ~~of interest~~ is presumed to be a bacterium belonging to a certain species of bacteria and the second, presumably metabolically similar microorganism is of the same species of bacteria, but the first and second microorganisms belong to different strains of the same species of bacteria.

29. (Currently amended) The method of claim 20 ~~where~~ wherein the second, presumably metabolically similar microorganism is a representative of a metabolic similarity group that exhibits a fingerprint spectrum that is closest in canonical variate or principal component space to the fingerprint spectrum exhibited by the first microorganism under the first set of environmental conditions. ~~of interest.~~

30. (Currently amended) The method of claim 29 ~~where~~ wherein the second, presumably metabolically similar microorganism is a distance-weighted composite of two or more representatives of metabolic similarity groups.

31. (Withdrawn, currently amended) The method of claim 20 ~~where~~ wherein the first set of environmental factors and the second set [[s]] of environmental factors comprise the same batch of the same growth medium and the first set of environmental factors and the second set of environmental factors differ in at least one parameter selected from the group consisting of temperature, pressure, exposure to light, and exposure to gases.

32. (Currently amended) The method of claim 20 ~~where~~ wherein the method is computer implemented.

33. (Withdrawn) A method of identifying a microorganism of interest, comprising:

culturing on a test growth medium a microorganism of interest and a second microorganism that is presumably metabolically similar to the microorganism of interest;

measuring a fingerprint spectrum of the microorganism of interest cultured on the test growth medium and a fingerprint spectrum of the second microorganism cultured on the test growth medium;

detecting differences between the fingerprint spectrum of the second microorganism cultured on the test growth medium and a fingerprint spectrum of the second microorganism cultured on a library growth medium;

using differences between the fingerprint spectra of the second microorganism cultured on the test and library growth media to transform the fingerprint spectrum of the microorganism of interest to an expected fingerprint spectrum for the microorganism of interest cultured on the library growth medium; and

detecting a similarity between the expected fingerprint spectrum and a library fingerprint spectrum of a known microorganism.

34. (Withdrawn) The method of claim 33 wherein the microorganism of interest is a bacterium and the second, presumably metabolically similar microorganism is a bacterium from a class of bacteria that are physiologically similar to the microorganism of interest.

35. (Withdrawn) The method of claim 33 wherein the presumably metabolically similar microorganism is a bacterium from the same bacterial genus as the microorganism of interest.

36. (Withdrawn) The method of claim 33, wherein the fingerprint spectra are selected from the group consisting of mass spectra, electron impact mass spectra, pyrolysis mass spectra, MAB mass spectra, MALDI mass spectra, infrared spectra, Fourier-transform infrared spectra, diffuse reflectance infrared spectra, attenuated total reflectance infrared spectra, ion-mobility spectra, gas chromatograms, fatty-acid methyl ester gas chromatograms, liquid chromatograms, and nuclear magnetic resonance spectra, and portions and combinations thereof.

37. (Withdrawn) The method of claim 33, wherein using differences between the fingerprint spectra of the second microorganism cultured on the test and library growth media

comprises using proportional differences between individual elements of the fingerprint spectra of the second microorganism between the test and library growth media that, when applied to individual elements of the fingerprint spectrum of the second microorganism cultured on the test growth medium, cause them to resemble corresponding elements of the fingerprint spectrum from the library growth medium.

38.  (Withdrawn) The method of claim 37, wherein using proportional differences between individual elements of each fingerprint spectrum comprises using proportional differences between each element of each fingerprint spectrum.

39.  (Withdrawn) A method for identifying an unknown microorganism, comprising:
    measuring a fingerprint spectrum of a microorganism that is presumably metabolically similar to the unknown microorganism and is cultured on a first growth medium;
    measuring fingerprint spectra for the unknown microorganism and the presumably metabolically similar microorganism cultured on a second growth medium;
    determining a transformation algorithm that converts the fingerprint spectrum of the presumably metabolically similar microorganism cultured on the second growth medium to its fingerprint spectrum when cultured on the first growth medium;
    using the transformation algorithm determined for the presumably metabolically similar organism to transform the fingerprint spectrum of the unknown microorganism cultured on the second growth medium into an expected fingerprint spectrum for the unknown microorganism cultured on the first growth medium; and,
    comparing the expected fingerprint spectrum of the unknown microorganism to fingerprint spectra of known microorganisms cultured on the first growth medium to identify the unknown microorganism.

40.  (Withdrawn) The method of claim 39 where determining the transformation algorithm comprises dividing the fingerprint spectrum of the presumably metabolically similar microorganism cultured on the first growth medium by its fingerprint spectrum when cultured on the second growth medium to yield a set of ratios.

41. (Withdrawn) The method of claim 40 where using the transformation algorithm comprises multiplying the fingerprint spectrum of the unknown microorganism by the set of ratios.

42. (Withdrawn) The method of claim 39 where comparing the expected fingerprint spectrum of the unknown microorganism comprises comparing to fingerprint spectra in a library database of fingerprint spectra that was assembled using the first growth medium.

43. (Withdrawn) The method of claim 42 where the comparison is accomplished using computer implemented pattern recognition.

44. (Withdrawn) The method of claim 39 where the unknown microorganism is a bacterium.

45. (Withdrawn) The method of claim 44 where the unknown microorganism is a bacterial pathogen and the metabolically similar microorganism is selected from the group consisting of *Salmonella* spp., *E. coli* strains, *Shigella* spp., *Yersinia enterocolitica, Aeromonas* spp., *Plesiomonas* spp., *Vibrio* spp., *Clostridium botulinum, Clostridium perfringens, Bacillus cereus, Listeria* spp., *Staphylococcus aureus, Staphylococcus species, Campylobacter jejuni* and other *Campylobacter* spp., and combinations thereof.

46. (Withdrawn) The method of claim 39 where the method is computer implemented.

47. (Withdrawn) The method of claim 39 where the fingerprint spectra are selected from the group consisting of mass spectra, electron impact mass spectra, pyrolysis mass spectra, MAB mass spectra, MALDI mass spectra, ESI mass spectra, infrared spectra, Fourier-transform infrared spectra, diffuse reflectance infrared spectra, attenuated total reflectance infrared spectra, ion-mobility spectra, gas chromatograms, fatty-acid methyl ester gas chromatograms, liquid chromatograms, and nuclear magnetic resonance spectra, and portions and combinations thereof.

Claims 48-66 (Canceled)

67. (Witdrawn, currently amended) The method of claim 20 ~~where~~ <u>wherein</u> the first and second sets of environmental factors comprise different growth media.

68. (Withdrawn, currently amended) The method of claim 20 ~~where~~ <u>wherein</u> the first and second sets of environmental factors comprise two batches of the same type of growth media.

69. (Currently amended) The method of claim 22 ~~where~~ <u>wherein</u> the fingerprint spectra are pyrolysis mass spectra.

70. (Currently amended) The method of claim 20, further comprising adding the expected spectrum of the <u>first</u> microorganism ~~of interest~~ to a database.

Please add following new claims 71-80.

--71. (New) The method of claim 31 wherein the first and second sets of environmental factors differ in temperature.

72. (New) A method for compensating for environmentally induced drift in fingerprint spectra that is due to differences in environment that affect the metabolic state of microorganisms, comprising:

deriving a relationship between a fingerprint spectrum of a first microorganism in a first environment and a fingerprint spectrum of the first microorganism in a second environment where differences between the first environment and the second environment affect the metabolic state of the first microorganism and a second, metabolically similar microorganism; and

applying the relationship derived for the first microorganism to transform a fingerprint spectrum of the second, metabolically similar microorganism in the first environment into a fingerprint spectrum of the second, metabolically similar microorganism in the second environment that is compensated for environmentally induced drift between the first environment and the second environment that is due to changes in environment that affect the metabolic state of the second microorganism.

73. (New) The method of claim 72 wherein the fingerprint spectra are selected from the group consisting of mass spectra, electron impact mass spectra, pyrolysis mass spectra, MAB mass spectra, MALDI mass spectra, ESI mass spectra, infrared spectra, Fourier-transform infrared spectra, diffuse reflectance infrared spectra, attenuated total reflectance infrared spectra, ion-mobility spectra, gas chromatograms, fatty-acid methyl ester gas chromatograms, liquid chromatograms, and nuclear magnetic resonance spectra, and portions and combinations thereof.

74. (New) The method of claim 72 further comprising a step of identifying the second microorganism by detecting a similarity between the fingerprint spectrum of the second microorganism in the second environment and a fingerprint spectrum of a known organism cultured in the second environmental.

75. (New) The method of claim 74 wherein detecting a similarity is accomplished by a pattern recognition method selected from the group consisting of statistical pattern recognition methods, artificial intelligence pattern recognition methods, and combinations thereof.

76. (New) The method of claim 72 wherein relationship derived for the first microorganism comprises proportional differences in individual elements of the fingerprint spectra of the first microorganism between the first environment and the second environment.

77. (New) The method of claim 72 wherein the first microorganism and the second, metabolically similar microorganism belong to a certain class of physiologically similar bacteria, but the first and second microorganisms belong to different genera of bacteria of the same class of physiologically similar bacteria.

78. (New) The method of claim 72 wherein the first microorganism and the second, metabolically similar microorganism belong to the same genus of bacteria, but the first microorganism and second, metabolically similar microorganism belong to different species of bacteria.

79. (New) The method of claim 72 wherein the first microorganism and the second, metabolically similar microorganism belong to the same species of bacteria, but the first

microorganism and second, metabolically similar microorganism belong to different strains of bacteria.

80.  (New) The method of claim 72 wherein the method is computer implemented.